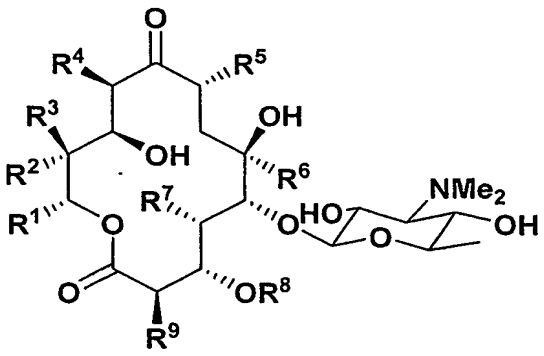
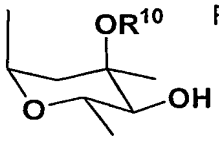
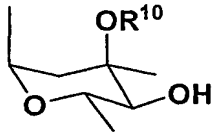
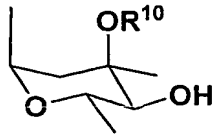
Figure 1A



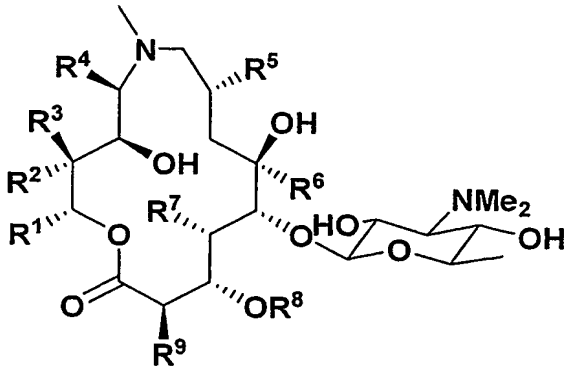
5-*O*-dedesosaminyl-5-*O*-mycaminosyl-erythromycin B
$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -H$ $R^8 =$  $R^{10} = CH_3$

5-*O*-dedesosaminyl-5-*O*-mycaminosyl-erythromycin A
$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -OH$ $R^8 =$  $R^{10} = CH_3$

5-*O*-dedesosaminyl-5-*O*-mycaminosyl-erythromycin C
$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -OH$ $R^8 =$  $R^{10} = H$

5

Figure 1B



5-*O*-dedesosaminyl-5-*O*-mycaminosyl-azithromycin

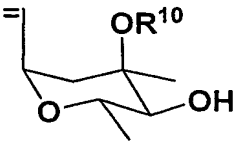
$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 =$ -OH $R^8 =$  $R^{10} = CH_3$

Figure 2

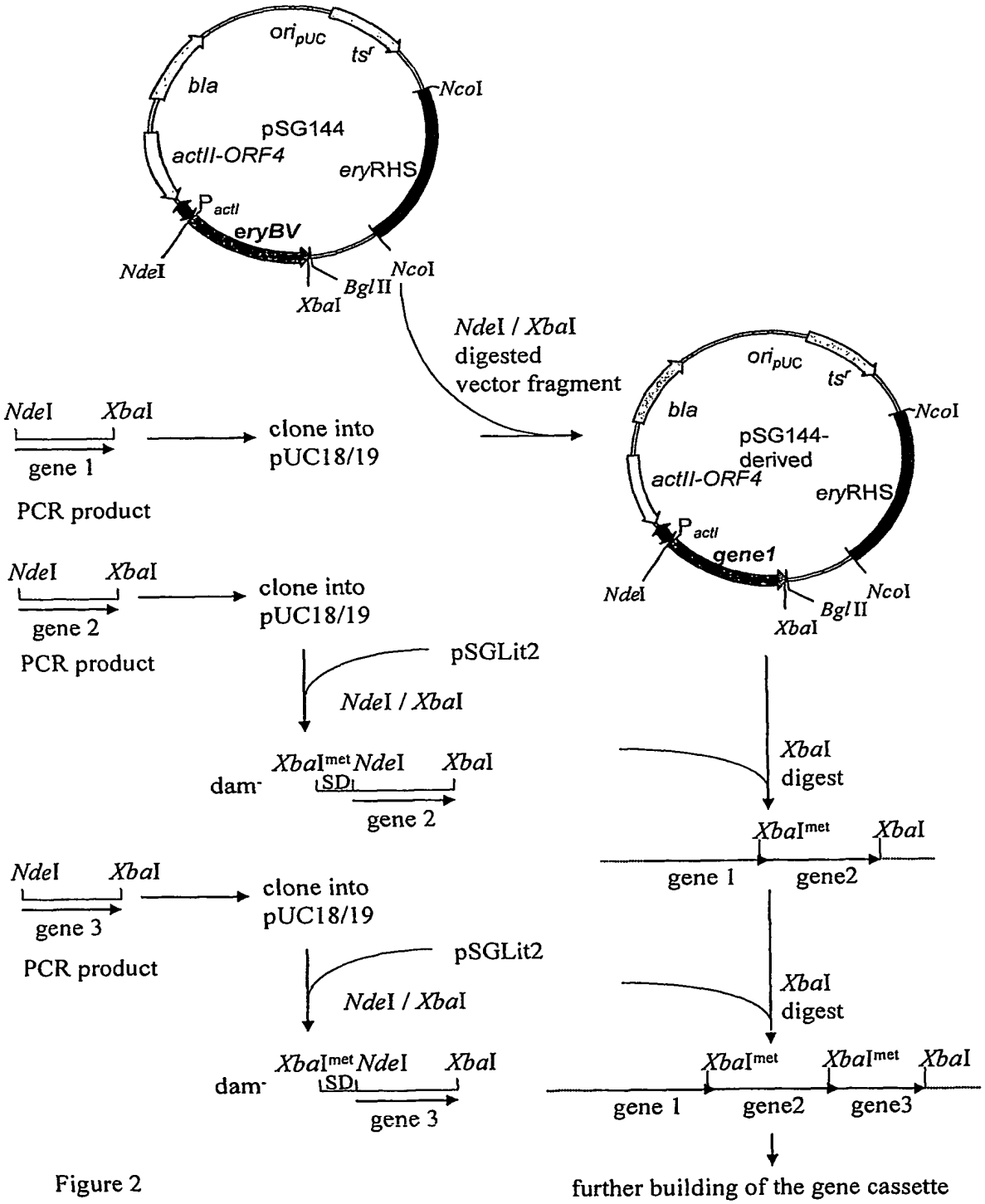


Figure 2

Figure 3

TylA1.pep x u08223.em_pro2

```
          .         .         .         .         .
    1 MNDRPRRAMKGIILAGGSGTRLRPLTGTLSKQLLPVYDKPMIYYPLSVLM 50
      |||||||||||||||||||||||||||||||||||||||||||||||||||
    1 MNDRPRRAMKGIILAGGSGTRLRPLTGTLSKQLLPVYDKPMIYYPLSVLM 50
          .         .         .         .         .
   51 LAGIREIQIISSKDHLDLFRSLLGEGDRLGLSISYAEQREPRGIAEAFLI 100
      |||||||||||||||||||||||||||||||||||||||||||||||||||
   51 LAGIREIQIISSKDHLDLFRSLLGEGDRLGLSISYAEQREPRGIAEAFLI 100
          .         .         .         .         .
  101 GARHIGGDDAALILGDNVFHGPGFSSVLTGTVARLDGCELFGYPVKDAHR 150
      |||||||||||||||||||||||||||||||||||||||||||||||||||
  101 GARHIGGDDAALILGDNVFHGPGFSSVLTGTVARLDGCELFGYPVKDAHR 150
          .         .         .         .         .
  151 YGVGEIDSGGRLLSLEEKPRRPRSNLAVTGLYLYTNDVVEIARTISPSAR 200
      ||||||||||||||||||||  ||||||||||||||||||||
  151 YGVGEIDSGGRLLSLEEKPRRPLEP.GRHRLYLYTNDVVEIARTISPSAR 199
          .         .         .         .         .
  201 GELEITDVNKVYLEQGRARLTELGRGFAWLDMGTHDSLLQAGQYVQLLEQ 250
      ||||||||||||||||||  |  ||||||||||||||||||||||||
  200 GELEITDVNKVYLEQGRA.AHGAGAVVAWLDMGTHDSLLQAGQYVQLLEQ 248
          .         .         .         .         .
  251 RQGERIACIEEIAMRMGFISAEQCYRLGQELRSSSYGSYIIDVAMRGAAA 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  249 RQGERIACIEEIAMRMGFISAEQCYRLGQELRSSSYGSYIIDVAMRGAAA 298

  301 DSRAQ 305
      |||||
  299 DSRAQ 303
```

Figure 4

TylAII.pep x u08223.em_pro2

```
          .         .         .         .         .
    1 MRVLVTGGAGFIGSHFTGQLLTGAYPDLGATRTVVLDKLTYAGNPANLEH 50
      ||||||||||||||||||||||| ||||||||||||||||||||||||||
    1 MRVLVTGGAGFIGSHFTGQLLTGAYPDLGATRTVVLDKLTYAGNPANLEH 50
          .         .         .         .         .
   51 VAGHPDLEFVRGDIADQALVRRLMEGVGLVVHFAAESHVDRSIESSEAFV 100
      |||||||||||||||||    || ||||||||||||||||||||||||||
   51 VAGHPDLEFVRGDIADHGWWRRLMEGVGLVVHFAAESHVDRSIESSEAFV 100
          .         .         .         .         .
  101 RTNVEGTRVLLQAAVDAGVGRFVHISTDEVYGSIAEGSWPEDHPLAPNSP 150
      |||||||||||||||||||||| |||||||||||||||||||.|||||
  101 RTNVEGTRVLLQAAVDAGVGRFVHISTDEVYGSIAEGSWPEDHPVAPNSP 150
          .         .         .         .         .
  151 YAATKAASDLLALAYHRTYGLDVRVTRCSNNYGPRQYPEKAVPLFTTNLL 200
      |||||||||||||||||||||| |||||||||||||||||||||||||||
  151 YAATKAASDLLALAYHRTYGLDVRVTRCSNNYGPRQYPEKAVPLFTTNLL 200
          .         .         .         .         .
  201 DGLPVPLYGDGGNTREWLHVDDHCRGVALVAAGGRPGVIYNIGGGTELTN 250
      |||||||||||||||||||||| ||||||| ||||||||||||||||||
  201 DGLPVPLYGDGGNTREWLHVDDHCRGVALVGAGGRPGVIYNIGGGTELTN 250
          .         .         .         .         .
  251 AELTDRILELCGADRSAVRRVADRPGHDRRYSVDTTKIREELGYAPRTGI 300
      |||||||||||||||||.||||| ||||||||||||||||||||||||||
  251 AELTDRILELCGADRSALRRVADRPGHDRRYSVDTTKIREELGYAPRTGI 300
          .         .         .
  301 TEGLAGTVAWYRDNRAWWEPLKRSPGGRELERA 333
      |||||||||||||||||||||| |||||||||
  301 TEGLAGTVAWYRDNRAWWEPLKRSPGGRELERA 333
```

Figure 5

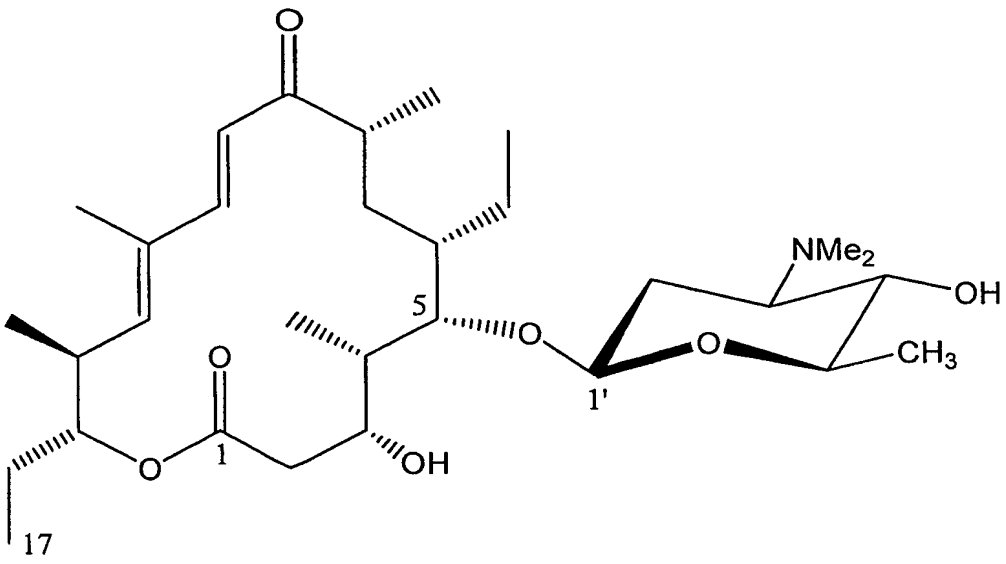
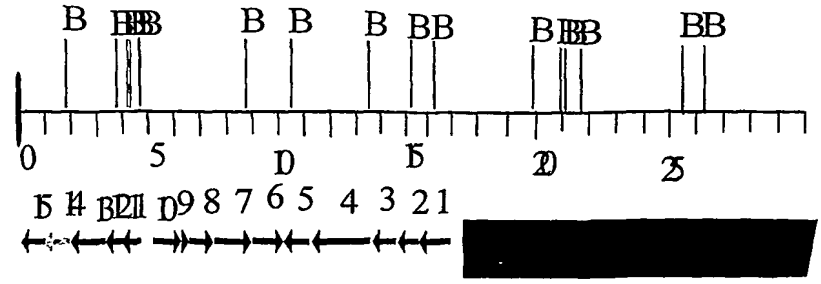
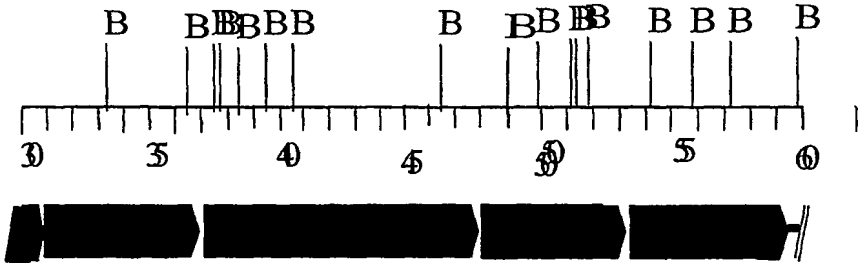


Figure 6





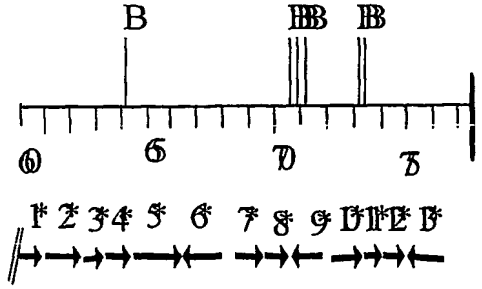


Figure 7

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   1 GGCATGCCTT CGGGGTGTGC GGCGGCGCCT CAGAGCGTGG CCAGTACCTC
  51 GTGCAGGGCC GCGATCACCT TGTCCTGTAC GTCGGGCGCG AGCCCCGGGT
 101 ACATCGGCAG CGAGAAGATC TCGTCCGCCA GCCGCTCCGT CACCGGCAGC
 151 GAGCCCTTGG CGTACCCCAG GTGCGCGAAG CCCGTCATGG TGTGCACGGG
 201 CCACGGGTAA CTGATGTTGA GCGAGATCCC GTACGACTTG AGCGCCTCGA
 251 TGATGTCGTC CCGGCGCGGG TGGCGGACGA CGTACACGTA ATACACGTGG
 301 TCGTTGCCCT CGGTGACGGA CGGCAGCACC AGGCCGCCGG GGCCCGTCAG
 351 GTTCGCGAGT CCTTCGGCGT AACGCCGGGC GACCGCGCGC CGGCCCTCGA
 401 TGTAGCGGTC GAGGCGGGTG AGCTTGCGGC GCAGGATCTC CGCCTGCACC
 451 TCGTCGAGCC GGCTGTTGTG GCCGGGCGTC TGCACGACGT AGTACACGTC
 501 CTCCATGCCG TAGTAGCGCA GCCGGCGCAG CGCACGGTCG ACGTCCGCGT
 551 CGTCGGTCAG CACGGCCCCG CCGTCGCCGT ACGCACCGAG GACCTTCGTC
 601 GGGTAGAACG AGAAGGCGGC GGCGTCGCCC AGCGTGCCGG CCAGCTCGCC
 651 GTGGTGGCGG GCACCGTGCG CCTGGGCGCA GTCCTCCAGC ACCACCAGGC
 701 CGTGCTGCTC GGCCAGGGCG CGCAAGGGCG CCATGTCGAC GCACTGCCCG
 751 TACAGGTGCA CCGGCAGCAG GGCCTTCGTG CGCGGGGTGA TGACGTCCGC
 801 GACCTGGTCG GTGTCCATGA GGTGGTCCTC GGCGCGGACG TCGACGAAGA
 851 CGGGCGTGGC ACCGGTGCCG TCGATGGCCA CCACCGTCGG CGCGGCCGTG
 901 TTGGAGACGG TGACGACCTC GTCCCCCGGG CCCACCCCGA GCGCCTGCAG
 951 ACCCAGCTTG ACGGCGTTGG TGCCGTTGTC GACACCGCCG CAGTGGCGCA
1001 GGCCGTGGTA GTCCGCGAAC TCCTTCTCGA ACCCGTCCAC GCTGGGGCCG
1051 AGGACCAACT GCCCGGAGGC GAAGACGGTC TCGACGGCGT CGAGGAGGTC
1101 CGCGCGTTCG TTCTGGTATT CCGCCAGGTA GTCCCAGACG TAGGTAGTCA
1151 CGGAGAGCTC AACCTCCAGA GTGTTTCGAT GGGGTGGTGG GAAGCCGGTG
1201 CGCGCGGACC AGGTCGTGCC AGCAGTCGCG GACCGACTCC CGCAGCGAAC
1251 GGCGCGGTGC CCAGCCCAGC AGGGCGCGCG CCGCGCCGGT GTCGACCCGC
1301 AGCCAGTCCT CCCGGTGCCC GGGAGCCCGG CCCGGAGCCG GGCGCTCCAC
1351 CACCCGCGCC GGAATGCCGC TCGCCTCGAT GAACAGGCCG ACCAGGTCGC
1401 GGACGGCGAC CGCCTCGCCC CGCCCGATGC CGACGGCGAC CGGGACGGCC
```

1451 GGTGCGCGGG CGGCGGCCAC GACGGCGTCG GCCACGTCCC GCACATCGAC

1501 GTAGTCCCGG TGCGCGCGCA GCCGGGACAG TTCCACGACG GCCTCCGCAC

1551 CCGTCCCGGC GGCCGCCAGC AGCCGCTCGG CGACCTGGCC CAGCAGACTG

1601 ATCCGCGGGG TGCCGGGGCC CGACACGTTG GACACCCGTA GCACCACACC

1651 GTCGACCCAC CCGCCCGAGG TGCCCCGCAG CACCGCCTCG CTGGCGGCGA

1701 GCTTGCTCCT GCCGTACGCC GTGTCCGGGC GCGGTACGGC GTCGGCGCCC

1751 ACCGAACCGC CGGGCGTCAC CGGGCCGTAC TCCAGTACCG AGCCGAGGTG

1801 GACCAGCCGC GGCCGCGCGG ACATCAGCGC CAGCGCCTCC AGCAGGCGCA

1851 GCGTGGGCAC CGCGGTGGCG GACCACATCT GCTCGTCGGT ACGGCCCCAG

1901 ATGCTTCCGA CGGAGTTGAC GATCGTGTCC GGACGCTCCG CGTCCAGGGC

1951 GGCGGCCAGC GCCGCGGGAT CCGTACCGGC CAGGTCCAGG GTGACGCAGC

2001 GGTACGGCAT CGGCTCCTCG GGCGGGCGGC GGCCCACCAC CACCACGTCA

2051 CGGCCCCGCG CGGCGAACGC CGCGCACACA TGCCGGCCGA CGTACCCGGC

2101 GCCGCCCAGG ACCACGACGC TGCCACTGCC ACTGCCGCGC GGCATCGGAT

2151 CGTTCACCAT

Figure 8

```
11301  CGTCAGTACA GCGTGTGGGC ACACGCCACC AGGGTGCGCA GCTCGATGTT
11351  GAGGTAGTTG CCGTGCGCCA GCAGCCCGGT GAGCTGACCG AGCGACAGCC
11401  AGGCGAAGTC GTCCGGTGCG TCCTCCGGGA AGTCGTGCGG GACCTCCACG
11451  ATCACGTAGC GGTTCTGGGC GTGGAAGAAG CGCCCGCCCT CCTCGGACTG
11501  GACGGCGTCG TAGCGCACGT CCTGAGGCGG CGCGGACAGC ACGTCCTCCA
11551  GGTACGGCGG GCCGGGCAGC CCCCGCGGAC CGGTGTGCTC CTGTGGCCGG
11601  CACTGGACCG TGGGGGCCAG CTCGGCGACG TTCAGGTGCC CGACGTCCAC
11651  CCGTGCCCGC ACGAGCGCGT GCAGCACGCC GTCGACGGAC TTGACCAGCA
11701  GCGCCATCAG ACCCGGCAGC CGCGGCTCGA TGAGCGGCTG CGTCCAGGAG
11751  GTGACCTCCC GGCTGCTGGC GCTGACCTCG GCGGCCATGA CCCGGAAGTG
11801  CCGCCCGCTC TCGTGGGCGA TCTCGTGCGG CGTGCGGTAC CAGCCGTCCG
11851  CCGTCACCGT ATCGAGCGGC ACCCGGTTCT GCACCAGCTC CCGCAGGGCG
11901  CGCACACCCG TGAACCACGT CAGGACCTCG GCCGTCGTGT GCCGCGCCGC
11951  ACCCGGCGAG CCGAAGAAGG AGCGCAGCAC GGGGGACGGG GCGGACGCGT
12001  CGGCGTCCGC CGTGGGCAGG CAGGCGAGGA TGGACCGGGC GTCCATGTTG
12051  ACCACGTTGT CCAGCATCAG CAGCCGGCGG AGCTGCCCCA GCGTCAGCCA
12101  GCGGAAGTCC TCCCCGATGT CGAGGTCGTC GTCCGCCGCC AACTCGACGA
12151  TCATGTTCCG GTTGCGTTTG GCCAGGACC AGTCCGCCTG TTCGGACTGG
12201  ATCGAGTCGA CCAGGACACG CGCCCGTCGC GGCCCCATGA ACAGGTCCAG
12251  ATAGCGGATG TCGCGCCCCC GGTGCACCCC GGTGAAGTTG CTCCGGGTGG
12301  CCTGCACGGT CGGCGACACC TGAAGAACGT TGACGTTCCC GGGCTCCATC
12351  TTGGCCTGCA TCAGGAAGTG CAGCACCCCG TCGATCTCCC GCGCCACGAT
12401  CCCGAGCAGC CCCACCTCCG GCTGCACCAT CATGGGCTGC CTCCACCCCC
12451  GCTCGGGCAG CCGGTCCGTA CGGACGTGCA GCCCCTCCAC GGAGAAGAAA
12501  CGGCCCGACG CGTGGTGCAG GTTTCCCGTA CCCGGGTGGA AGCTCCAGCC
12551  GCGCAGCTCC GCGAAGGGAA CGCGGGACAC GTCGAAGCGC CCCGCCCGCA
12601  GGCGTTCGGC CAGCCAGCCG GAGATGCCGT CGAACGGCGT GACCGCACTG
12651  TCCGCGGTGC GTGCCGACAC CAGCACCCGC CGCGCCGTGT CCACCGGGTC
12701  ACCGGGCCGG ACCGCGTCCG CACGGCGCCG CGCGGCGCCG TGCGGGGCGG
```

12751 GGGCGGATCG CGGCGGTACG GGTTCGCGGG CGGTGTCCGC GGCGGTGCGC

12801 GGCGGGACGG GGCCGGTGCT CGTGTCCGCG GCGGTACGCG GTGGGACGGT

12851 CCCGGTGGCC GTGTCCGCGG TGGCCGTGCC GGCGAGGGCG TCGCCGATGG

12901 TCCGGCACAC CTCGTCCATC CGGTCGTTCA GATAGAAGTG ACCGCCGGCG

12951 AAGGTGTGCA GGGCGAAGGG GCCCGTGGTC AGCTCCCGCC AGGCCCTCGC

13001 CTCCTCCAGC GGGACATCGG GATCACGGTC ACCGGTGAGC ACCGTGACCG

13051 GACAGTCCAG CGCACCGCCG GGCACATACG CGTACGTGCC CGCCGCCCGG

13101 TAGTCGTTGC GGATCGCCGG CAGGGCCAGC CGCAGCAGCT CCTCGTCCTG

13151 GAGGACGGCG TCCTCGGTGC CCTGAAGCGT GGCGATCTCC GCGATCAGCG

13201 CGTCGTCGTC GAGGAGGTGG GCGACGTCCC GCCGGCGCAC CGTCGGCGCA

13251 CGGCGGCCCG ACACCAGCAG ATGGACGGGG GAGGCCTGCC CGGAACCGCG

13301 CAGCCGGCGC GCGACCTCGA ACGCCACCGT GGCACCCATG CTGTGCCCGA

13351 ACAGCGCGAG CGGACGGTCG GCCCAGCGCA GGATCTCCGG CACCACCTGG

13401 TCCACCAGGC CCGATATGGA CGGGATGAAC GGCTCGTGCC GGCGGTCCTG

13451 GCGGCCCGGG TACTGCACCG CCAGCGCCTC CACGGTCTCG TCCAGTCCGC

13501 GTGCCAGGGC GGCGAAGGAG GTCGCGGCGC CACCGGCGTG CGGGAAGCAG

13551 ACCAGACGCA GTTCCGGATC CCGCACCGGG CGGTAACGGC GGACCCACAG

13601 ACCCTCGTCC GGGTGTCCGG CCGGCGACGG GGCTCCCGGA ACGGGTGGTG

13651 CGGAAGGGGT GCTCACGGCG GATCCAGCTC CTCGCGGTCG GGGGGACCGC

13701 TGTCGGGGAC GGCACGTCGG GTGCGGACGT CGGGTACGGG CGTCGGGGCG

13751 TGACGGGGAG GGACGGGGCG GTCGGTCAGT CGGTGCGCCG GGCCTCCTGC

13801 GCGGCCTTCT TCAGCGGTTC CCACCACGCG CGGTTCTCCG CGTACCAGCG

13851 CACCGTGTCC GCCAGGCCCG TCGTGAAGTC CGTACGCGGG GCATAGCCCA

13901 GCTCGCCCGT GATCTTGCCG ATGTCCAGCG CGTACCGCAG GTCGTGCCCC

13951 GGCCGGTCGG CGACGTGGCG CACCGACGAG GCGTCGGCAC CGCACAGCCC

14001 GAGCAGCCGC TTCGTCAGCT CCCGGTTGGT CAGCTCCGTC CCGCCACCGA

14051 TGTGGTAGAC CTCGCCCGGG CGCCCGCGGG TCGCCACCAG GCTGATCCCG

14101 CGGCAGTGGT CGTCCACGTG CAGCCAGTCC CGGCTGTTGC CGCCGTCGCT

14151 GTACAGCGGC ACCGTCAGAC CGTCCAACAG GTTCGTGGCG AAGAGCGGGA

14201 CGACCTTCTC GGGGTGCTGG TACGGGCCGT AGTTGTTGGA GCACCGGGTG

14251 ACGACGACCG GCAGGCCGTA CGTCCGGTGG TAGGCCAGCG CCAGGAGGTC

14301 CGACGCCGCC TTCGAGGCGG CGTACGGGGA GTTCGGCGCC AGCGGCTGCT

14351 CCTCGCGCCA CGACCCCTCG GCGATCGAGC CGTACACCTC GTCCGTGGAG

14401 ACGTGGACGA ACCGGCCGGC CCCCGCCTCC ACCGCGGCCT GCAAGAGGAC

14451 TTGCGTCCCC CGTACGTTCG TCTCGACGAA CGCCGACGCG TCGGCGATGG

14501 AGCGGTCCAC GTGCGACTCC GCCGCGAAGT GGACCACGAC GTCCGCCCCC

14551 CGCACGACCC GGGACATCAC CTCCGCGTCC CGGATGTCGG CGTGCACGAA

14601 CTCCAGCGAC GGATGGTCCG CGACCGGGTC CAGGTTGGCG AGGTTCCCGG

14651 CATAGGTCAG CTTGTCGACC ACCACCGTCC GCGCCCCGGC CAGGTCCGGA

14701 TACGCCCCGG CCAGCAGTTG TCTGACGAAG TGCGAGCCGA TGAAGCCCGC

14751 ACCTCCGGTG ACCAGCAGCC GCATGGGAGC ACAGACCTTT CTTCCAGGGA

14801 CGGGAAACGG GGAGGCGGAC GGGGACGGAG GCGAGGGCGG TGGCTATGCG

14851 GCCGGTCCGG ACATGAGGGT CTCCGCCACG TCCATCAAGT ACCGGCCGTA

14901 GCTGGAGCTC TCGAGTTCAC GGCCGAGCTC GTGGCACTGC CGCGCGCTGA

14951 TGTACCCCAT CCGCAGGGCG ATCTCCTCGA CGCAGGAGAT CCGCACGCCC

15001 TGCCGCTGCT CCAGGAGCTG GACGTACTGC CCCGCTTGCA GCAGCGAGCT

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15251 GCTTCTCCTC CAGGGACACC AGCCGGCCTT CCGCGTCGAC CTCGCCGACG

15301 CCGTAGCGCC GGGGGTCCTT CACCGGGTAG CCGAACAGCT CGCAGCCGTC

15351 CAGCCGCGCC GCGGTGGAGG CCAGCACGGA GGAGAACCCC GGACCGTGGA

15401 AGACGTTGTC CCCCAGGATG AGGGCGACCG GGTCGTCCCC GATGTGCTCC

15451 TCGCCGATGA GGAACGCCTC GGCGATGCCC CGGGGCTCCT CCTGCTCGGC

15501 GTAGCCGACA CTGATCCCGA TGCGGCTGCC GTCGCCCAGC AGCGAACGGA

15551 ACATCTCCAA GTGCGTCTTC GACGTGATGA TCTGGATGTC CCGGATCCCC

15601 GCCAGCATGA GCACCGACAG CGGGTAGTAG ATCATGGGCT TGTCGTAGAC

15651 CGGCAGCAAC TGCTTGGACA GTGCCCCGGT CAGGGGGCGC AGGCGCGTGC

15701 CGCTGCCGCC CGCCAGGATG ATGCCCTTCA TGGGCCGCCG GTCCGCCGTC

15751 GTCTTCGTCA T

Figure 9

```
59800                                                                G
59801  TGAGCCCCGC ACCCGCCACC GAGGACCCGG CCGCCGCCGG GCGCCGCCTG
59851  CAACTGACCC GCGCAGCCCA GTGGTTCGCG GGAACCCAGG ACGACCCGTA
59901  CGCGCTCGTC CTGCGCGCCG AGGCCACCGA CCCGGCCCCG TACGAGGAGC
59951  GGATCCGGGC CCACGGGCCG CTCTTCCGCA GCGACCTGCT CGACACCTGG
60001  GTCACGGCGA GCAGGGCCGT CGCCGACGAA GTGATCACCT CACCCGCCTT
60051  CGACGGGCTC ACGGCCGACG GGCGGCGCCC CGGCGCGCGG GAACTGCCGC
60101  TGTCCGGCAC CGCGCTCGAC GCGGACCGCG CCACATGCGC ACGGTTCGGG
60151  GCCCTCACCG CCTGGGGCGG GCCGCTGCTG CCGGCGCCGC ACGAGCGGGC
60201  GCTGCGCGAG TCCGCCGAAC GGCGGGCCCA CACACTCCTC GACGGGGCGG
60251  AGGCCGCCCT GGCCGCCGAC GGCACCGTCG ACCTCGTCGA CGCGTACGCC
60301  CGCAGGCTCC CCGCGCTGGT CCTCCGCGAA CAGCTCGGCG TGCCGGAGGA
60351  GGCGGCGACC GCCTTCGAGG ACGCGCTGGC CGGCTGCCGC CGCACCCTGG
60401  ACGGCGCCCT GTGCCCGCAA CTCCTCCCGG ACGCCGTGGC GGGGGTGCGC
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60601  CTGGCGCGTC CCGCGCAGTG GGCGGAGCTC GTACGCGACC CGCGCCTCGC
60651  GGCCGCCGCG GTGACCGAAA CGCTGCGTGT CGCCCCGCCC GTCCGCCTGG
60701  AGCGGCGGGT CGCCCGCGAG GACACGGACA TCGCCGGGCA GCGCCTCCCC
60751  GCCGGGGGGA GCGTCGTGAT CCTCGTCGCC GCCGTCAACC GCGCGCCCGT
60801  ATCCGCGGGA AGCGACGCCT CCACCACCGT CCCGCACGCC GGCGGCCGGC
60851  CCCGTACCTC CGCCCCCTCC GTCCCCTCAG CCCCCTTCGA CCTCACACGG
60901  CCCGTGGCCG CGCCCGGGCC GTTCGGGCTC CCCGGCGACC TGCACTTCCG
60951  CCTCGGCGGG CCCCTGGTCG GAACGGTCGC CGAAGCCGCG CTCGGTGCGC
61001  TGGCCGCACG GCTCCCCGGT CTGCGCGCCG CCGGGCCGGC CGTGCGGCGC
61051  CGCCGCTCAC CGGTGCTGCA CGGACACGCC CGCCTCCCCG TCGCCGTCGC
61101  CCGGACGGCC CGTGACCTGC CCGCCACCGC ACCGCGGAAC TGAGGAGGGA
61151  GTGCCCCGAT GCGTATCCTG CTGACGTCGT TCGCGCACAA CACGCACTAC
```

61201 TACAACCTGG TCCCCCTCGG CTGGGCGCTG CGCGCCGCCG GGCACGACGT

61251 ACGGGTCGCC AGCCAGCCCT CGCTGACCGG CACCATCACC GGCTCCGGGC

61301 TGACCGCCGT CCCCGTGGGC GACGACACGG CCATCGTCGA GCTGATCACC

61351 GAGATCGGCG ACGACCTCGT CCTCTACCAG CAGGGCATGG ACTTCGTGGA

61401 CACCCGCGAC GAGCCGCTGT CCTGGGAACA CGCCCTCGGA CAGCAGACGA

61451 TCATGTCGGC CATGTGCTTC TCGCCGCTGA ACGGCGACAG CACCATCGAC

61501 GACATGGTGG CGCTGGCCCG TTCCTGGAAA CCGGACCTCG TCCTGTGGGA

61551 GCCCTTCACC TACGCGGGAC CCGTCGCCGC GCACGCCTGC GGCGCCGCCC

61601 ACGCCCGGCT GCTGTGGGGT CCCGACGTGG TCCTCAACGC ACGGCGGCAG

61651 TTCACCCGGC TGCTCGCCGA GCGCCCCGTC GAACAGCGCG AGGACCCGGT

61701 CGGCGAATGG CTCACGTGGA CGCTGGAGCG CCACGGCCTC GCCGCCGACG

61751 CGGACACGAT CGAGGAACTG TTCGCCGGGC AGTGGACGAT CGACCCCAGC

61801 GCCGGGAGCC TGCGGCTGCC GGTCGACGGC GAGGTCGTGC CCATGCGCTT

61851 CGTGCCGTAC AACGGCGCCT CGGTCGTCCC CGCCTGGCTC TCCGAGCCGC

61901 CTGCCCGGCC CCGGGTCTGC GTCACCCTCG GCGTCTCCAC CCGGGAGACC

61951 TACGGCACGG ACGGCGTCCC GTTCCACGAA CTGCTGGCCG GACTGGCCGA

62001 CGTGGACGCC GAGATCGTCG CCACCCTCGA CGCGGGGCAG CTCCCGGACG

62051 CCGCCGGTCT GCCCGGCAAT GTGCGCGTCG TCGACTTCGT GCCGCTGGAC

62101 GCCCTGCTGC CGAGCTGCGC CGCGATCGTC CACCACGGAG GCGCGGGAAC

62151 CTGTTTCACG GCCACCGTGC ACGGCGTCCC GCAGATCGTC GTGGCCTCCC

62201 TCTGGGACGC GCCGCTGAAG GCGCACCAAC TCGCCGAGGC GGGCGCCGGG

62251 ATCGCCCTGG ACCCCGGGGA ACTGGGCGTG GACACCCTGC GCGGCGCCGT

62301 CGTGCGGGTG CTGGAGAGCC GCGAGATGGC CGTGGCGGCG CGTCGCCTCG

62351 CCGACGAGAT GCTCGCCGCC CCCACCCCGG CCGCGCTCGT CCCCCGCCTC

62401 GAACGCCTCA CCGCCGCGCA CCGCCGCGCC TGATCCCGCC AAGGAGCCCC

62451 CATGAACCTC GAATACAGCG GCGACATCGC CCGGTTGTAC GACCTGGTCC

62501 ACCAGGGAAA GGGCAAGGAC TACCGGGCGG AGGCCGAGGA GCTGGCCGCG

62551 CTTGTCACCC AGCGCCGCCC CGGGGCCCGC TCCCTCCTCG ACGTGGCCTG

62601 CGGAACGGGG ATGCACCTGC GGCACCTCGG CGACCTCTTC GAGGAGGTGG

62651 CCGGGGTGGA GATGTCCCCC GACATGCTGG CCATCGCGCA GCGGCGCAAC

62701 CCGGAGGCCG GCATCCACCG GGGGGACATG CGGGACTTCG CCCTCGGCCG

62751 CCGCTTCGAC GCCGTGATCT GCATGTTCAG TTCCATCGGG CACATGCGCG

62801 ACCAGCGGGA ACTGGACGCG GCGATCGGCC GGTTCGCCGC GCACCTGCCG

62851 TCCGGCGGGG TCGTGATCGT CGATCCCTGG TGGTTCCCGG AGACGTTCAC

62901 ACCGGGGTAC GTCGGCGCGA GCCTCGTCGA GGCCGAGGGC CGCACCATCG

62951 CGCGCTTCTC CCACTCCGCG CTCGAGGACG GCGCGACCCG GATCGATGTG

63001 GACTACCTCG TCGGCGTGCC GGGGGAGGGG GTGCGGCACT TGAAGGAGAC

63051 CCATCGGATC ACGCTTTTCG GGCGTGCGCA GTACGAGGCG GCCTTCACCG

63101 CGGCGGGGAT GTCCGTCGAG TACCTCCCGC ACGCCGCCAC CGACCGCGGA

63151 CTCTTCGTCG GCGTCCAGGC CTGA

Figure 10

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  1  MKGIILAGGS GTRLRPLTGA LSKQLLPVYD KPMIYYPLSV LMLAGIRDIQ
 51  IITSKTHLEM FRSLLGDGSR IGISVGYAEQ EEPRGIAEAF LIGEEHIGDD
101  PVALILGDNV FHGPGFSSVL ASTAARLDGC ELFGYPVKDP RRYGVGEVDA
151  EGRLVSLEEK PEKPRSHLAV TGLYFYDNGV VDIARRLTPS PRGELEITDV
201  NKVYLEQGRA RMTELGRGFA WLDMGTHSSL LQAGQYVQLL EQRQGVRISC
251  VEEIALRMGY ISARQCHELG RELESSSYGR YLMDVAETLM SGPAA
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Figure 11

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   1  MRLLVTGGAG FIGSHFVRQL LAGAYPDLAG ARTVVVDKLT YAGNLANLDP
  51  VADHPSLEFV HADIRDAEVM SRVVRGADVV VHFAAESHVD RSIADASAFV
 101  ETNVRGTQVL LQAAVEAGAG RFVHVSTDEV YGSIAEGSWR EEQPLAPNSP
 151  YAASKAASDL LALAYHRTYG LPVVVTRCSN NYGPYQHPEK VVPLFATNLL
 201  DGLTVPLYSD GGNSRDWLHV DDHCRGISLV ATRGRPGEVY HIGGGTELTN
 251  RELTKRLLGL CGADASSVRH VADRPGHDLR YALDIGKITG ELGYAPRTDF
 301  TTGLADTVRW YAENRAWWEP LKKAAQEARR TD
```

Figure 12

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   1  VSTPSAPPVP GAPSPAGHPD EGLWVRRYRP VRDPELRLVC FPHAGGAATS
  51  FAALARGLDE TVEALAVQYP GRQDRRHEPF IPSISGLVDQ VVPEILRWAD
 101  RPLALFGHSM GATVAFEVAR RLRGSGQASP VHLLVSGRRA PTVRRRDVAH
 151  LLDDDALIAE IATLQGTEDA VLQDEELLRL ALPAIRNDYR AAGTYAYVPG
 201  GALDCPVTVL TGDRDPDVPL EEARAWRELT TGPFALHTFA GGHFYLNDRM
 251  DEVCRTIGDA LAGTATADTA TGTVPPRTAA DTSTGPVPPR TAADTAREPV
 301  PPRSAPAPHG AARRRADAVR PGDPVDTARR VLVSARTADS AVTPFDGISG
 351  WLAERLRAGR FDVSRVPFAE LRGWSFHPGT GNLHHASGRF FSVEGLHVRT
 401  DRLPERGWTQ PIIVQPEVGL LGIVAREIDG VLHFLMQAKM EPGNVNVLQV
 451  SPTVQATRSN FTGVHRGRDI RYLDLFMGPR RARVLVDSIQ SEQADWFLAK
 501  RNRNMIVELA ADDDLDIGED FRWLTLGQLR RLLMLDNVVN MDARSILACL
 551  PTADADASAP SPVLRSFFGS PGAARHTTAE VLTWFTGVRA LRELVQNRVP
 601  LDTVTADGWY RTPHEIAHES GRHFRVMAAE VSASSREVTS WTQPLIEPRL
 651  PGLMALLVKS VDGVLHALVR ARVDVGHLNV AELAPTVQCR PQEHTGPRGL
 701  PGPPYLEDVL SAPPQDVRYD AVQSEEGGRF FHAQNRYVIV EVPHDFPEDA
 751  PDDFAWLSLG QLTGLLAHGN YLNIELRTLV ACAHTLY
```

Figure 13

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   1  MVNDPMPRGS GSGSVVVLGG AGYVGRHVCA AFAARGRDVV VVGRRPPEEP
  51  MPYRCVTLDL AGTDPAALAA ALDAERPDTI VNSVGSIWGR TDEQMWSATA
 101  VPTLRLLEAL ALMSARPRLV HLGSVLEYGP VTPGGSVGAD AVPRPDTAYG
 151  RSKLAASEAV LRGTSGGWVD GVVLRVSNVS GPGTPRISLL GQVAERLLAA
 201  AGTGAEAVVE LSRLRAHRDY VDVRDVADAV VAAARAPAVP VAVGIGRGEA
 251  VAVRDLVGLF IEASGIPARV VERPAPGRAP GHREDWLRVD TGAARALLGW
 301  APRRSLRESV RDCWHDLVRA HRLPTTPSKH SGG
```

Figure 14

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   1  VTTYVWDYLA EYQNERADLL DAVETVFASG QLVLGPSVDG FEKEFADYHG
  51  LRHCGGVDNG TNAVKLGLQA LGVGPGDEVV TVSNTAAPTV VAIDGTGATP
 101  VFVDVRAEDH LMDTDQVADV ITPRTKALLP VHLYGQCVDM APLRALAEQH
 151  GLVVLEDCAQ AHGARHHGEL AGTLGDAAAF SFYPTKVLGA YGDGGAVLTD
 201  DADVDRALRR LRYYGMEDVY YVVQTPGHNS RLDEVQAEIL RRKLTRLDRY
 251  IEGRRAVARR YAEGLANLTG PGGLVLPSVT EGNDHVYYVY VVRHPRRDDI
 301  IEALKSYGIS LNISYPWPVH TMTGFAHLGY AKGSLPVTER LADEIFSLPM
 351  YPGLAPDVQD KVIAALHEVL ATL
```

Figure 15

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  1  VSPAPATEDP AAAGRRLQLT RAAQWFAGTQ DDPYALVLRA EATDPAPYEE
 51  RIRAHGPLFR SDLLDTWVTA SRAVADEVIT SPAFDGLTAD GRRPGARELP
101  LSGTALDADR ATCARFGALT AWGGPLLPAP HERALRESAE RRAHTLLDGA
151  EAALAADGTV DLVDAYARRL PALVLREQLG VPEEAATAFE DALAGCRRTL
201  DGALCPQLLP DAVAGVRAEA ALTAVLASAL RGTPAGRAPD AVAAARTLAV
251  AAAEPAATLV GNAVQELLAR PAQWAELVRD PRLAAAAVTE TLRVAPPVRL
301  ERRVAREDTD IAGQRLPAGG SVVILVAAVN RAPVSAGSDA STTVPHAGGR
351  PRTSAPSVPS APFDLTRPVA APGPFGLPGD LHFRLGGPLV GTVAEAALGA
401  LAARLPGLRA AGPAVRRRRS PVLHGHARLP VAVARTARDL PATAPRN
```

Figure 16

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   1  MRILLTSFAH NTHYYNLVPL GWALRAAGHD VRVASQPSLT GTITGSGLTA
  51  VPVGDDTAIV ELITEIGDDL VLYQQGMDFV DTRDEPLSWE HALGQQTIMS
 101  AMCFSPLNGD STIDDMVALA RSWKPDLVLW EPFTYAGPVA AHACGAAHAR
 151  LLWGPDVVLN ARRQFTRLLA ERPVEQREDP VGEWLTWTLE RHGLAADADT
 201  IEELFAGQWT IDPSAGSLRL PVDGEVVPMR FVPYNGASVV PAWLSEPPAR
 251  PRVCVTLGVS TRETYGTDGV PFHELLAGLA DVDAEIVATL DAGQLPDAAG
 301  LPGNVRVVDF VPLDALLPSC AAIVHHGGAG TCFTATVHGV PQIVVASLWD
 351  APLKAHQLAE AGAGIALDPG ELGVDTLRGA VVRVLESREM AVAARRLADE
 401  MLAAPTPAAL VPRLERLTAA HRRA
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Figure 17

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  1  MNLEYSGDIA RLYDLVHQGK GKDYRAEAEE LAALVTQRRP GARSLLDVAC
 51  GTGMHLRHLG DLFEEVAGVE MSPDMLAIAQ RRNPEAGIHR GDMRDFALGR
101  RFDAVICMFS SIGHMRDQRE LDAAIGRFAA HLPSGGVVIV DPWWFPETFT
151  PGYVGASLVE AEGRTIARFS HSALEDGATR IDVDYLVGVP GEGVRHLKET
201  HRITLFGRAQ YEAAFTAAGM SVEYLPHAAT DRGLFVGVQA
```